



SEQUENCE LISTING

RECEIVED  
FEB 15 2002  
TECH CENTER 1600/2900

<110> Immusol Incorporated  
Welch, Peter J.  
Barber, Jack R.

<120> Tumor Suppressor Molecules and Methods  
of Use

<130> 039316-0301

<140> US 09/438,917

<141> 1999-11-12

<160> 20

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<211> 16

<212> RNA

<213> Artificial Sequence

<220>

<223> hairpin ribozyme

<400> 1

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<223> n = A,U,C or G

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16

AI  
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<221> CDS

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 ggaagcggcg gacgcaggag gcctcgtgga ggacacagca gc atg gga cag tca 114  
 Met Gly Gln Ser

<sup>1</sup>  
 M G A S

ggg agg tcc cgg cac cag aag cgc gcc ccg ccc cag gcg cag ctc cgc 162  
 Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln Ala Gln Leu Arg

<sup>5</sup> G R S R H <sup>10</sup> Q K R A P <sup>15</sup> Q A Q L R <sup>20</sup>

aac ctc gag gcc tat gcc gcg aac ccg cac tcg ttc gtg ttc acg cga 210  
 Asn Leu Glu Ala Tyr Ala Ala Asn Pro His Ser Phe Val Phe Thr Arg

N L E A <sup>25</sup> Y A A N P <sup>30</sup> H S F V F <sup>35</sup> T R

ggc tgc acg ggt cgc aac atc cgg cag ctc agc ctg gac gtg cgg cgg 258  
 Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu Asp Val Arg Arg  
 G C T <sup>40</sup> G R N I R <sup>45</sup> Q L S L D <sup>50</sup> V R R  
 gtc atg gag ccc gtc act gcc agc cgt ctg cag gtt cgt aag aag aac 306  
 Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val Arg Lys Lys Asn  
 V M <sup>55</sup> E P V T A <sup>60</sup> S R L Q V <sup>65</sup> R L L N  
 tcg ctg aag gac tgc gtg gca gtg gct ggg ccc ctc ggg gtc aca cac 354  
 Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His  
 S <sup>70</sup> L K D C V A <sup>75</sup> V A G P <sup>80</sup> L G V T H  
 ttt ctg atc cta gca aaa caa gag acc aat gtc tac ttt aag ctg atg 402  
 Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr Phe Lys Leu Met  
<sup>85</sup> F L I L A <sup>90</sup> K Q E T N <sup>95</sup> V Y F K L <sup>100</sup> M  
 cgc ctc cca gga ggc ccc acc ttg acc ttc cag gtc aag aag tac tcg 450  
 Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val Lys Lys Tyr Ser  
 R L P G <sup>105</sup> P T V T <sup>110</sup> F Q V K K <sup>115</sup> S  
 ctg gtg cgt gat gtg gtc tcc tca ctg cgc cgg cac cgc atg cac gag 498  
 Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His Arg Met His Glu  
 L V R <sup>120</sup> V V S S <sup>125</sup> R R H R <sup>130</sup> M H E  
 cag cag ttt gcc cac cca ccc ctc ctg gta ctc aac agc ttt ggc ccc 546  
 Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro  
 Q Q <sup>135</sup> F A H P P <sup>140</sup> L L V L N <sup>145</sup> S F G P  
 cat ggt atg cat gtg aag ctc atg gcc acc atg ttc cag aac ctg ttc 594  
 His Gly Met His Val Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe  
 H <sup>150</sup> G M H V K <sup>155</sup> L M A T M <sup>160</sup> F Q D L F  
 ccc tcc atc aac gtg cac aag gtg aac ctg aac acc atc aag cgc tgc 642  
 Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr Ile Lys Arg Cys  
<sup>165</sup> P S I N V <sup>170</sup> H K V N L <sup>175</sup> N T I K R <sup>180</sup> C  
 ctc ctc atc gac tac aac ccc gac tcc cag gag ctg gac ttc cgc cac 690  
 Leu Leu Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His  
 L L I D <sup>185</sup> T N P D S <sup>190</sup> Q E L D F <sup>195</sup> R H  
 tat agc atc aaa gtt gtt cct gtg ggc gcg agt cgc ggg atg aag aag 738  
 Tyr Ser Ile Lys Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys  
 Y S I K <sup>200</sup> V V P V <sup>205</sup> G A S R G <sup>210</sup> M K K  
 ctg ctc cag gag aag ttc ccc aac atg agc cgc ctg cag gac atc agc 786  
 Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser  
 L L <sup>215</sup> Q Q L F P <sup>220</sup> N M S R L <sup>225</sup> Q D I S  
 gag ctg ctg gcc acg ggc gcg ggg ctg tcg gag agc gag gca gag cct 834  
 Glu Leu Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser Glu Ala Glu Pro  
 Q <sup>230</sup> L A T G A <sup>235</sup> G L S E S <sup>240</sup> Q A E P

AI  
 Conf

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Asp	Gly	Asp	His	Asn	Ile	Thr	Glu	Leu	Pro	Gln	Ala	Val	Ala	Gly	Arg	
245	G		H		250			L	P	255	A	V	A		R	260
ggc	aac	atg	cgg	gcc	cag	cag	agt	gca	gtg	cgg	ctc	acc	gag	atc	ggc	930
Gly	Asn	Met	Arg	Ala	Gln	Gln	Ser	Ala	Val	Arg	Leu	Thr	Glu	Ile	Gly	
	G	N	M		265		S	A	V		L				275	
ccg	cgg	atg	aca	ctg	cag	ctc	atc	aag	gtc	cag	gag	ggc	gtc	ggg	gag	978
Pro	Arg	Met	Thr	Leu	Gln	Leu	Ile	Lys	Val	Gln	Glu	Gly	Val	Gly	Glu	
	P	R	M		280				285	V				290		
ggc	aaa	gtg	atg	ttc	cac	agt	ttt	gtg	agc	aag	acg	gag	gag	gag	ctg	1026
Gly	Lys	Val	Met	Phe	His	Ser	Phe	Val	Ser	Lys	Thr	Glu	Glu	Glu	Leu	
	G		295	V	M	F		S	300	F	V		L		305	
cag	gcc	atc	ctg	gaa	gcc	aag	gag	aag	aag	ctg	cgg	ctg	aag	gct	cag	1074
Gln	Ala	Ile	Leu	Glu	Ala	Lys	Glu	Lys	Lys	Leu	Arg	Leu	Lys	Ala	Gln	
	310		L		A		315		L	L			320			
agg	cag	gcc	cag	cag	gcc	cag	aat	gtg	cag	cgc	aag	cag	gag	cag	cgg	1122
Arg	Gln	Ala	Gln	Gln	Ala	Gln	Asn	Val	Gln	Arg	Lys	Gln	Glu	Gln	Arg	
325		A			330		N	V		335	L				340	
R																
gag	gcc	cac	aga	aag	aag	agc	ctg	gag	ggc	atg	aag	aag	gca	cgg	gtc	1170
Glu	Ala	His	Arg	Lys	Lys	Ser	Leu	Glu	Gly	Met	Lys	Lys	Ala	Arg	Val	
	A	P	R	345	K	S	L	G	350	M	R	K	A		355	
ggg	ggt	agt	gat	gaa	gag	gcc	tct	ggg	atc	cct	tca	agg	acg	gcg	agc	1218
Gly	Gly	Ser	Asp	Glu	Glu	Ala	Ser	Gly	Ile	Pro	Ser	Arg	Thr	Ala	Ser	
		S	360	E	E	A	S	365		P	S	R	370	A		
ctg	gag	ttg	ggt	gag	gac	gat	gat	gaa	cag	gaa	gat	gat	gac	atc	gag	1266
Leu	Glu	Leu	Gly	Glu	Asp	Asp	His	Glu	Gln	Glu	Asp	Asp	Asp	Ile	Glu	
	L		375	E			380						385	I		
tat	ttc	tgc	cag	gcg	gtg	ggc	gag	gcg	ccc	agt	gag	gac	ctg	ttc	ccc	1314
Tyr	Phe	Cys	Gln	Ala	Val	Gly	Glu	Ala	Pro	Ser	Glu	Asp	Leu	Phe	Pro	
	390			A	V	395	E	A	P	S	400		L	F	P	
gag	gcc	aag	cag	aaa	cgg	ctt	gcc	aag	tct	cca	ggg	cgg	aag	cgg	aag	1362
Glu	Ala	Lys	Gln	Lys	Arg	Leu	Ala	Lys	Ser	Pro	Gly	Arg	Lys	Arg	Lys	
405	A	L		L	410	L	A	L	S	P		R		R	420	
cgg	tgg	gaa	atg	gat	cga	ggc	agg	ggt	cgc	ctt	tgt	gac	cag	aag	ttt	1410
Arg	Trp	Glu	Met	Asp	Arg	Gly	Arg	Gly	Arg	Leu	Cys	Asp	Gln	Lys	Phe	
	R		M	425	R	G	R	G	430	L	C				435	
ccc	aag	acc	aag	gac	aag	tcc	cag	gga	gcc	cag	gcc	agg	cgg	ggg	ccc	1458
Pro	Lys	Thr	Lys	Asp	Lys	Ser	Gln	Gly	Ala	Gln	Ala	Arg	Arg	Gly	Pro	
	P			440				445	A		A	R	R	450		

aga ggg gct tcc cgg gat ggt ggg cga ggc cgg ggc cga ggc cgc cca 1506  
 Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly Arg Gly Arg Pro  
 455 460 465

ggg aag aga gtg gcc tga g cccaagccgc accggagcag cggctggatt 1555  
 Gly Lys Arg Val Ala \*  
 470

gaacgccccca gattggggcc cgagatgtgg ccctcggttt cctttcataa aggagttgtg 1615  
 tccccagccc ttccactcca gtaaagaact gaattggcaa aaaaaaaaaa 1664

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 Val Phe Thr Arg Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu  
 35 40 45  
 Asp Val Arg Arg Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val  
 50 55 60  
 Arg Lys Lys Asn Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu  
 65 70 75 80  
 Gly Val Thr His Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr  
 85 90 95  
 Phe Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val  
 100 105 110  
 Lys Lys Tyr Ser Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His  
 115 120 125  
 Arg Met His Glu Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn  
 130 135 140  
 Ser Phe Gly Pro His Gly Met His Val Lys Leu Met Ala Thr Met Phe  
 145 150 155 160  
 Gln Asn Leu Phe Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr  
 165 170 175  
 Ile Lys Arg Cys Leu Leu Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu  
 180 185 190  
 Asp Phe Arg His Tyr Ser Ile Lys Val Val Pro Val Gly Ala Ser Arg  
 195 200 205  
 Gly Met Lys Lys Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu  
 210 215 220  
 Gln Asp Ile Ser Glu Leu Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser  
 225 230 235 240  
 Glu Ala Glu Pro Asp Gly Asp His Asn Ile Thr Glu Leu Pro Gln Ala  
 245 250 255

Val Ala Gly Arg Gly Asn Met Arg Ala Gln Gln Ser Ala Val Arg Leu  
 260 265 270  
 Thr Glu Ile Gly Pro Arg Met Thr Leu Gln Leu Ile Lys Val Gln Glu  
 275 280 285  
 Gly Val Gly Glu Gly Lys Val Met Phe His Ser Phe Val Ser Lys Thr  
 290 295 300  
 Glu Glu Glu Leu Gln Ala Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg  
 305 310 315 320  
 Leu Lys Ala Gln Arg Gln Ala Gln Gln Ala Gln Asn Val Gln Arg Lys  
 325 330 335  
 Gln Glu Gln Arg Glu Ala His Arg Lys Lys Ser Leu Glu Gly Met Lys  
 340 345 350  
 Lys Ala Arg Val Gly Gly Ser Asp Glu Glu Ala Ser Gly Ile Pro Ser  
 355 360 365  
 Arg Thr Ala Ser Leu Glu Leu Gly Glu Asp Asp Asp Glu Gln Glu Asp  
 370 375 380  
 Asp Asp Ile Glu Tyr Phe Cys Gln Ala Val Gly Glu Ala Pro Ser Glu  
 385 390 395 400  
 Asp Leu Phe Pro Glu Ala Lys Gln Lys Arg Leu Ala Lys Ser Pro Gly  
 405 410 415  
 Arg Lys Arg Lys Arg Trp Glu Met Asp Arg Gly Arg Gly Arg Leu Cys  
 420 425 430  
 Asp Gln Lys Phe Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala  
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AI  
CMT  
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Al  
Cuk

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 Thr Ala Arg Gly Gln Trp Gly Ala Gly Gln Pro Glu Asp Glu Glu Asp  
 370 375 380  
 Asp Ala Glu Tyr Phe Arg Gln Ala Val Gly Glu Pro Asp Glu Asp  
 385 390 395 400  
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 405 410 415  
 Lys Lys Gln Arg Gly Phe Glu Gln Arg Pro Gly Asn Lys  
 420 425

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 Ile His Arg Gly Leu Ala Cys Pro Tyr Ile Thr Asp Leu Thr Leu Asp  
 35 40 45  
 Phe Arg Arg Ile Met Glu Pro Phe Thr Ala Ser Asn Leu Arg Glu Lys  
 50 55 60  
 Arg Met Asn Arg Ile Gln Asp Phe Val Cys Leu Ser Ser Phe Phe His  
 65 70 75 80  
 Val Ser His Met Gly Ile Phe Asn Lys Ala Ser Ile Gln Leu Ser Phe  
 85 90 95  
 Lys Val Val Arg Leu Pro Arg Gly Pro Ser Leu Thr Phe Lys Val His  
 100 105 110  
 Gln Phe Thr Leu Ala Arg Asp Val Ile Ser Leu Ser Lys Lys Gln Met  
 115 120 125  
 Ile Asp Asn Asp His Phe Lys His Ala Pro Leu Val Ile Met Asn Asn  
 130 135 140  
 Phe Ser Gly Asp Gly Lys His Leu Lys Leu Met Ala Thr Thr Phe Gln  
 145 150 155 160  
 Asn Met Phe Pro Ser Ile Asn Leu Ala Thr Val Asn Ile Gly Thr Ile  
 165 170 175  
 Arg Arg Cys Val Leu Phe Ser Tyr Asn Pro Asp Thr Lys Leu Val Glu  
 180 185 190  
 Met Arg His Tyr Ser Val Gln Val Val Pro Val Gly Leu Lys Arg Ala  
 195 200 205  
 Val Gln Lys Ile Val Lys Gly Thr Val Pro Asn Leu Gly Lys Cys Asn  
 210 215 220  
 Glu Val Val Asp Phe Val Thr Lys Asp Gly Tyr Ala Ser Glu Ser Glu  
 225 230 235 240  
 Ala Glu Asp Asp Glu Gln Ser His Val Val Leu Ala Gln Thr Leu Lys  
 245 250 255  
 Ser Lys Gly Asn Leu Glu Asp Lys Lys Ser Ser Ile Lys Leu His Glu  
 260 265 270

Ile	Gly	Pro	Arg	Leu	Thr	Met	Gln	Leu	Ile	Lys	Ile	Glu	Glu	Gly	Leu
	275						280					285			
Leu	Thr	Gly	Glu	Val	Leu	Tyr	His	Cys	His	Val	Val	Lys	Thr	Glu	Asp
	290					295					300				
Glu	Lys	Glu	Thr	Leu	Arg	Lys	Leu	Val	Glu	Lys	Lys	Arg	Lys	Gln	Lys
305					310					315				320	
Glu	Gln	Arg	Lys	Lys	Glu	Gln	Ala	Glu	Asn	Arg	Ala	Phe	Asn	Leu	Lys
			325						330					335	
Leu	Lys	Lys	Asp	Glu	Lys	Trp	Ala	Ala	Lys	Arg	Ala	Ala	Glu	Gly	Arg
			340					345					350		
Thr	Asp	Ser	Asp	Pro	Glu	Asp	Asp	Ala	Glu	Tyr	Tyr	Lys	Glu	Glu	Val
	355					360						365			
Gly	Glu	Glu	Pro	Asp	Glu	Glu	Leu	Phe	Lys	Met	Glu	Ala	Lys	Ser	Ser
	370					375					380				
Arg	Lys	Arg	Pro	Ser	Leu	Gly	Gly	Gly	Met	Lys	Tyr	Lys	Asn	Lys	Arg
385					390					395					400
Ala	Lys	Leu	Asp	Thr	Lys	Asp	Lys	Asn	Asp	Lys	Ser	Glu	Arg	Thr	Asp
			405						410					415	
Phe	Tyr	Asp	Arg	Lys	Cys	Lys	Phe	Asp	Arg	Lys	Asp	Lys	Lys	Asp	Lys
			420					425					430		
Phe	Asp	Pro	Lys	Asn	Gly	Arg	Ala	Lys	Phe	Asp	Pro	Lys	Asn	Lys	Arg
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Ala	Lys	Phe	Asp	His	Pro	Lys	Ser	Arg	Lys	Ser	Lys				
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15

<210> 19  
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 <213> mus musulus

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 <223> Xaa = Any Amino Acid

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			20					25					30		
Tyr	Ala	Ala	Gln	Pro	His	Ser	Phe	Val	Phe	Thr	Arg	Gly	Arg	Ala	Gly
		35					40						45		

Arg Asn Val Arg Gln Leu Ser Leu Asp Val Arg Arg Val Met Glu Pro  
 50 55 60  
 Leu Thr Ala Thr Arg Leu Gln Val Arg Lys Lys Asn Ser Leu Lys Asp  
 65 70 75 80  
 Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His Phe Leu Ile Leu  
 85 90 95  
 Thr Lys Thr Asp Asn Ser Val Tyr Leu Lys Leu Met Arg Leu Pro Gly  
 100 105 110  
 Gly Pro Thr Leu Thr Phe Gln Ile Ser Lys Tyr Thr Leu Ile Arg Asp  
 115 120 125  
 Val Val Ser Ser Leu Arg Arg His Arg Met His Glu Gln Gln Phe Asn  
 130 135 140  
 His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro Gln Gly Met His  
 145 150 155 160  
 Ile Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe Pro Ser Ile Asn  
 165 170 175  
 Val His Thr Val Asn Leu Asn Thr Ile Lys Arg Cys Leu Leu Ile Asn  
 180 185 190  
 Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His Tyr Ser Val Lys  
 195 200 205  
 Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys Leu Leu Gln Glu  
 210 215 220  
 Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser Glu Leu Leu Ala  
 225 230 235 240  
 Thr Gly Val Gly Leu Ser Asp Ser Glu Val Glu Pro Asp Gly Glu His  
 245 250 255  
 Asn Thr Thr Glu Leu Pro Gln Ala Val Ala Gly Arg Gly Asn Met Gln  
 260 265 270  
 Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly Pro Arg Met Thr  
 275 280 285  
 Leu Gln Leu Ile Lys Ile Gln Glu Gly Val Gly Asn Gly Asn Val Leu  
 290 295 300  
 Phe His Ser Phe Val His Lys Thr Glu Glu Glu Leu Gln Ala Ile Leu  
 305 310 315 320  
 Ala Ala Lys Glu Glu Lys Leu Arg Leu Lys Ala Gln Arg Gln Asn Gln  
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<220>  
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 <223> Xaa = Any Amino Acid

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 Phe Gly Val Lys Lys Tyr Ser Leu Val Arg Asp Val Val Ser Ser Leu  
 35 40 45  
 Arg Arg His Arg Met His Glu Gln Gln Phe Ala His Pro Pro Leu Leu  
 50 55 60  
 Val Leu Asn Ser Phe Gly Pro His Gly Met His Val Lys Leu Met Ala  
 65 70 75 80  
 Thr Met Phe Gln Asn Leu Phe Pro Ser Ile Asn Val His Lys Val Asn  
 85 90 95  
 Leu Asn Thr Ile Lys Arg Cys Ser Ser Xaa Asp Leu Lys Pro Gly Phe  
 100 105 110  
 Pro Arg Ser Leu Asp Phe Arg Pro Ile Ile Ala Phe Lys Gly Gly Ser  
 115 120 125  
 Cys Trp Ala Pro Asn Ser Gly Gly Leu  
 130 135

AI  
 M

ORIGINAL US.  
SER 1ST



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Marked-up copy

SEQUENCE LISTING

<110> Welch, Peter J.  
Barber, Jack R.

<120> Tumor Suppressor Molecules and Methods  
of Use

<130> P-IU 3446

<140> US 09/438,917

<141> 1999-11-12

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 16

<212> RNA

<213> Artificial Sequence

<220>

<223> hairpin ribozyme

<400> 1

acctccccag aacctt

"u" instead of "T"

16

<210> 2

<211> 16

<212> RNA

<213> homo sapiens

<220>

<221> misc\_feature

<222> (1)...(16)

<223> n = A,T,C or G

"u"

<400> 2

aggngtgcgg ggaggt

"u"

16

<210> 3

<211> 16

<212> RNA

<213> Artificial Sequence

<220>

<223> hairpin ribozyme

<400> 3

agagtgaag aaacta

"u"

16

<210> 4  
<211> 16  
<212> RNA  
<213> homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(16)  
<223> n = A,T,C or G

<400> 4  
tagtngtcta cactct

16

<210> 5  
<211> 1664  
<212> DNA  
<213> homo sapiens

<220>  
<221> CDS  
<222> (103)...(1525)

<400> 5  
gcttgatgtc gtcccacgcc gtgccggctc tcaggcgccg gaagtgaagt ggcacacggcc 60  
ggaagcggcg gacgcaggag gcctcgtgga ggacacagca gc atg gga cag tca 114  
Met Gly Gln Ser  
1

ggg agg tcc cgg cac cag aag cgc gcc ccg ccc cag gcg cag ctc cgc 162  
Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln Ala Gln Leu Arg  
5 10 15 20

aac ctc gag gcc tat gcc gcg aac ccg cac tcg ttc gtg ttc acg cga 210  
Asn Leu Glu Ala Tyr Ala Ala Asn Pro His Ser Phe Val Phe Thr Arg  
25 30 35

ggc tgc acg ggt cgc aac atc cgg cag ctc agc ctg gac gtg cgg cgg 258  
Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu Asp Val Arg Arg  
40 45 50

gtc atg gag ccc gtc act gcc agc cgt ctg cag gtt cgt aag aag aac 306  
Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val Arg Lys Lys Asn  
55 60 65

tcg ctg aag gac tgc gtg gca gtc gct ggg ccc ctc ggg gtc aca cac 354  
Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His  
70 75 80

ttt ctg atc cta gca aaa caa gag acc aat gtc tac ttt aag ctg atg 402  
Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr Phe Lys Leu Met  
85 90 95 100

cgc ctc cca gga ggc ccc acc ttg acc ttc cag gtc aag aag tac tcg	450
Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val Lys Lys Tyr Ser	
105 110 115	
ctg gtg cgt gat gtg gtc tcc tca ctg cgc cgg cac cgc atg cac gag	498
Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His Arg Met His Glu	
120 125 130	
cag cag ttt gcc cac cca ccc ctc ctg gta ctc aac agc ttt ggc ccc	546
Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro	
135 140 145	
cat ggt atg cat gtg aag ctc atg gcc acc atg ttc cag aac ctg ttc	594
His Gly Met His Val Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe	
150 155 160	
ccc tcc atc aac gtg cac aag gtg aac ctg aac acc atc aag cgc tgc	642
Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr Ile Lys Arg Cys	
165 170 175 180	
ctc ctc atc gac tac aac ccc gac tcc cag gag ctg gac ttc cgc cac	690
Leu Leu Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His	
185 190 195	
tat agc atc aaa gtt gtt cct gtg ggc gcg agt cgc ggg atg aag aag	738
Tyr Ser Ile Lys Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys	
200 205 210	
ctg ctc cag gag aag ttc ccc aac atg agc cgc ctg cag gac atc agc	786
Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser	
215 220 225	
<del>gag ctg ctg gcc acg ggc gcg ggg ctg tcc gag agc gag gca gag cct</del>	<del>834</del>
<del>Glu Leu Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser Glu Ala Glu Pro</del>	
<del>230 235 240</del>	
gac ggc gac cac aac atc aca gag ctg cct cag gct gtc gct ggc cgt	882
Asp Gly Asp His Asn Ile Thr Glu Leu Pro Gln Ala Val Ala Gly Arg	
245 250 255 260	
ggc aac atg cgg gcc cag cag agt gca gtg cgg ctc acc gag atc ggc	930
Gly Asn Met Arg Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly	
265 270 275	
ccg cgg atg aca ctg cag ctc atc aag gtc cag gag ggc gtc ggg gag	978
Pro Arg Met Thr Leu Gln Leu Ile Lys Val Gln Glu Gly Val Gly Glu	
280 285 290	
ggc aaa gtg atg ttc cac agt ttt gtg agc aag acg gag gag gag ctg	1026
Gly Lys Val Met Phe His Ser Phe Val Ser Lys Thr Glu Glu Glu Leu	
295 300 305	
cag gcc atc ctg gaa gcc aag gag aag aag ctg cgg ctg aag gct cag	1074



Gln Ala Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg Leu Lys Ala Gln  
 310 315 320

agg cag gcc cag cag gcc cag aat gtg cag cgc aag cag gag cag cgg 1122  
 Arg Gln Ala Gln Gln Ala Gln Asn Val Gln Arg Lys Gln Glu Gln Arg  
 325 330 335 340

gag gcc cac aga aag aag agc ctg gag ggc atg aag aag gca cgg gtc 1170  
 Glu Ala His Arg Lys Lys Ser Leu Glu Gly Met Lys Lys Ala Arg Val  
 345 350 355

ggg ggt agt gat gaa gag gcc tct ggg atc cct tca agg acg gcg agc 1218  
 Gly Gly Ser Asp Glu Glu Ala Ser Gly Ile Pro Ser Arg Thr Ala Ser  
 360 365 370

ctg gag ttg ggt gag gac gat cat gaa cag gaa gat gat gac atc gag 1266  
 Leu Glu Leu Gly Glu Asp Asp His Glu Gln Glu Asp Asp Asp Ile Glu  
 375 380 385

tat ttc tgc cag gcg gtg ggc gag gcg ccc agt gag gac ctg ttc ccc 1314  
 Tyr Phe Cys Gln Ala Val Gly Glu Ala Pro Ser Glu Asp Leu Phe Pro  
 390 395 400

gag gcc aag cag aaa cgg ctt gcc aag tct cca ggg cgg aag cgg aag 1362  
 Glu Ala Lys Gln Lys Arg Leu Ala Lys Ser Pro Gly Arg Lys Arg Lys  
 405 410 415 420

cgg tgg gaa atg gat cga ggc agg ggt cgc ctt tgt gac cag aag ttt 1410  
 Arg Trp Glu Met Asp Arg Gly Arg Gly Arg Leu Cys Asp Gln Lys Phe  
 425 430 435

ccc aag aca aag gac aag tcc cag gga gcc cag gcc agg cgg ggg ccc 1458  
 Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala Arg Arg Gly Pro  
 440 445 450

aga ggg gct tcc cgg gat ggt ggg cga ggc cgg ggc cga ggc cgc cca 1506  
 Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly Arg Gly Arg Pro  
 455 460 465

ggg aag aga gtg gcc tga g cccaagccgc accggagcag cggctggatt 1555  
 Gly Lys Arg Val Ala \*

470

gaacgccccca gattggggcc cgagatgtgg ccctcggttt cctttcataa aggagttgtg 1615  
 tccccagccc ttccactcca gtaaagaact gaattggcaa aaaaaaaaaa 1664

<210> 6

<211> 473

<212> PRT

<213> homo sapiens

<400> 6

Met Gly Gln Ser Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln

1	5	10	15
Ala Gln Leu Arg Asn Leu Glu Ala Tyr Ala Ala Asn Pro His Ser Phe			
20	25	30	
Val Phe Thr Arg Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu			
35	40	45	
Asp Val Arg Arg Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val			
50	55	60	
Arg Lys Lys Asn Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu			
65	70	75	80
Gly Val Thr His Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr			
85	90	95	
Phe Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val			
100	105	110	
Lys Lys Tyr Ser Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His			
115	120	125	
Arg Met His Glu Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn			
130	135	140	
Ser Phe Gly Pro His Gly Met His Val Lys Leu Met Ala Thr Met Phe			
145	150	155	160
Gln Asn Leu Phe Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr			
165	170	175	
Ile Lys Arg Cys Leu Leu Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu			
180	185	190	
Asp Phe Arg His Tyr Ser Ile Lys Val Val Pro Val Gly Ala Ser Arg			
195	200	205	
Gly Met Lys Lys Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu			
210	215	220	
Gln Asp Ile Ser Glu Leu Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser			
225	230	235	240
Glu Ala Glu Pro Asp Gly Asp His Asn Ile Thr Glu Leu Pro Gln Ala			
245	250	255	
Val Ala Gly Arg Gly Asn Met Arg Ala Gln Gln Ser Ala Val Arg Leu			
260	265	270	
Thr Glu Ile Gly Pro Arg Met Thr Leu Gln Leu Ile Lys Val Gln Glu			
275	280	285	
Gly Val Gly Glu Gly Lys Val Met Phe His Ser Phe Val Ser Lys Thr			
290	295	300	
Glu Glu Glu Leu Gln Ala Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg			
305	310	315	320
Leu Lys Ala Gln Arg Gln Ala Gln Gln Ala Gln Asn Val Gln Arg Lys			
325	330	335	
Gln Glu Gln Arg Glu Ala His Arg Lys Lys Ser Leu Glu Gly Met Lys			
340	345	350	
Lys Ala Arg Val Gly Gly Ser Asp Glu Glu Ala Ser Gly Ile Pro Ser			
355	360	365	
Arg Thr Ala Ser Leu Glu Leu Gly Glu Asp Asp His Glu Gln Glu Asp			
370	375	380	
Asp Asp Ile Glu Tyr Phe Cys Gln Ala Val Gly Glu Ala Pro Ser Glu			
385	390	395	400
Asp Leu Phe Pro Glu Ala Lys Gln Lys Arg Leu Ala Lys Ser Pro Gly			
405	410	415	
Arg Lys Arg Lys Arg Trp Glu Met Asp Arg Gly Arg Gly Arg Leu Cys			
420	425	430	

Asp Gln Lys Phe Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala  
435 440 445  
Arg Arg Gly Pro Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly  
450 455 460  
Arg Gly Arg Pro Gly Lys Arg Val Ala  
465 470

<210> 7  
<211> 87  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic oligonucleotides

<221> misc\_feature  
<222> (1)...(87)  
<223> n = A,T,C or G

<400> 7  
cgcgtagcag gtaatatacc acggaccgaa gtccgtgtgt ttctctggtn nnnttctnnn 60  
nnnnnggatc ctgtttccgc ccggttt 87

<210> 8  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic oligonucleotide

<400> 8  
gtccgtggta tattacctgg ta 22

<210> 9  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic oligonucleotide

<400> 9  
cgaaaccggg cggaacagg 20

<210> 10  
<211> 52  
<212> RNA  
<213> Artificial Sequence

<220>  
<223> hairpin ribozyme

<221> misc\_feature  
<222> (1)...(52)  
<223> n = A,T,C or G

<400> 10  
nnnnnnnnag aannnnnacca gagaaacaca cguuguggua uauuaccugg ua 52

<210> 11  
<211> 27  
<212> DNA  
<213> homo sapien<sup>S</sup>

<400> 11  
ccatcctaatac gactcact atagggc 27

<210> 12  
<211> 43  
<212> DNA  
<213> homo sapien<sup>S</sup>

<220>  
<221> misc\_feature  
<222> (1)...(42)  
<223> n = A,T,C or G

<400> 12  
cgatgctcct ctagactcga gggtaccacc tccccgacnc cct 43

<210> 13  
<211> 38  
<212> DNA  
<213> Artificial Sequence

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<220>  
<223> primer

<400> 13  
ggccacgcgt cgactagtag tttttttttt tttttttv 38

<210> 14  
<211> 20  
<212> DNA  
<213> homo sapien<sup>S</sup>

<400> 14  
cggctcaccg agatcggccc 20

<210> 15  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>

<223> primer

<400> 15

ggccacgcgt cgactagta c t

21

<210> 16

<211> 429

<212> PRT

<213> mus musculus

<400> 16

Met	Gly	Gln	Ser	Gly	Arg	Ser	Arg	His	Gln	Lys	Arg	Asn	Arg	Ala	Gln	1	5	10	15
Ala	Gln	Leu	Arg	Asn	Leu	Glu	Ser	Tyr	Ala	Ala	Gln	Pro	His	Ser	Phe	20	25	30	
Val	Phe	Thr	Arg	Gly	Arg	Ala	Gly	Arg	Asn	Val	Arg	Gln	Leu	Ser	Leu	35	40	45	
Asp	Val	Arg	Arg	Val	Met	Glu	Pro	Leu	Thr	Ala	Thr	Arg	Leu	Gln	Val	50	55	60	
Arg	Lys	Lys	Asn	Ser	Leu	Lys	Asp	Cys	Val	Ala	Val	Ala	Gly	Pro	Leu	65	70	75	80
Gly	Val	Thr	His	Phe	Leu	Ile	Leu	Thr	Lys	Thr	Cys	Asn	Ser	Val	Tyr	85	90	95	
Leu	Lys	Leu	Met	Arg	Leu	Pro	Gly	Gly	Pro	Thr	Leu	Thr	Phe	Gln	Ile	100	105	110	
Ser	Lys	Tyr	Thr	Leu	Ile	Arg	Asp	Val	Val	Ser	Ser	Leu	Arg	Arg	His	115	Phe 120	125	
Arg	Met	His	Glu	Gln	Gln	Pro	Asn	His	Pro	Pro	Leu	Leu	Val	Leu	Asn	130	135	140	
Ser	Phe	Gly	Pro	Gln	Ala	Met	His	Ile	Lys	Leu	Met	Ala	Thr	Met	Phe	145	150	155	160
Gln	Asn	Leu	Phe	Pro	Ser	Ile	Asn	Val	His	Thr	Val	Asn	Leu	Asn	Thr	165	170	Gln 175	
Ile	Lys	Arg	Cys	Leu	Leu	Ile	Asn	Tyr	Asn	Pro	Asp	Ser	Cys	Glu	Leu	180	185	190	
Asp	Phe	Arg	His	Tyr	Ser	Val	Lys	Val	Val	Pro	Val	Gly	Ala	Ser	Arg	195	200	205	
Gly	Met	Lys	Lys	Leu	Leu	Gln	Glu	Lys	Phe	Pro	Asn	Met	Ser	Arg	Leu	210	215	g 220	
Gln	Asp	Ile	Ser	Glu	Leu	Leu	Ala	Thr	Gln	Val	Gly	Leu	Ser	Asp	Ser	225	230	↑ 235	240
Glu	Val	Glu	Pro	Asp	Gln	Glu	His	Asn	Ile	Thr	Glu	Leu	Pro	Gln	Ala	245	Py 250	Thr 255	
Val	Ala	Gly	Arg	Gly	Asn	Met	Gln	Ala	Gln	Gln	Ser	Ala	Val	Arg	Leu	260	265	270	
Thr	Glu	Ile	Gly	Pro	Arg	Met	Thr	Leu	Gln	Leu	Ile	Lys	Ile	Gln	Glu	275	Asn 280	285	
Gly	Val	Gly	Glu	Gly	Asn	Val	Leu	Phe	His	Ser	Phe	Val	His	Lys	Thr	290	295	300	
Glu	Glu	Glu	Leu	Gln	Ala	Ile	Leu	Ala	Ala	Lys	Glu	Glu	Lys	Leu	Arg	305	310	315	320
Leu	Lys	Ala	Gln	Arg	Gln	Asn	Gln	Gln	Ala	Glu	Asn	Leu	Gln	Phe	Ser	325	330	335	

Arg Ser Cys Arg Gly Pro Gln Glu Glu Glu Pro Gly Arg His Lys Ala  
 340 345 350  
 Ser Pro Cys Lys Gly Arg Arg Glx Gln Glx Cys Glx Gly Pro Arg Gly  
 355 360 365  
 Thr Ala Arg Gly Gln Trp Gly Ala Gly Gln Pro Glu Asp Glu Glu Asp  
 370 375 380  
 Asp Ala Glu Tyr Phe Arg Gln Ala Val Gly Glu Glu Pro Asp Glu Asp  
 385 390 395 400  
 Leu Phe Pro Thr Ala Ala Lys Arg Arg Arg Gln Gly Gly Leu Leu Ala  
 405 410 415  
 Lys Lys Gln Arg Gly Phe Glu Gln Arg Pro Gly Asn Lys  
 420 425

<210> 17  
 <211> 460  
 <212> PRT  
 <213> Drosophila

<400> 17

Met Gly Gly Lys Lys Lys Val His Pro Lys Thr Arg Thr Ala Ala Phe  
 1 5 10 15  
 Lys Ala Ser Glu Pro Ser Glu Ile Val Glu Ala Pro His Ser Phe Val  
 20 25 30  
 Ile His Arg Gly Leu Ala Cys Pro Tyr Ile Thr Asp Leu Thr Leu Asp  
 35 40 45  
 Phe Arg Arg Ile Met Glu Pro Phe Thr Ala Ser Asn Leu Arg Glu Lys  
 50 55 60  
 Arg Met Asn Arg Ile Gln Asp Phe Val Cys Leu Ser Ser Phe Phe His  
 65 70 75 80  
 Val Ser His Met Gly Ile Phe Asn Lys Ala Ser Thr Gln Leu Ser Phe  
 85 90 95  
 Lys Val Val Arg Leu Pro Arg Gly Pro Ser Leu Thr Phe Lys Val His  
 100 105 110  
 Gln Phe Thr Leu Ala Arg Asp Val Ile Ser Leu Ser Lys Lys Gln Met  
 115 120 125  
 Ile Asp Asn Asp His Phe Lys His Ala Pro Leu Val Ile Met Asn Asn  
 130 135 140  
 Phe Ser Gly Asp Gly Lys His Leu Lys Leu Met Ala Thr Thr Phe Gln  
 145 150 155 160  
 Asn Met Phe Pro Ser Ile Asn Leu Ala Thr Val Asn Ile Gly Thr Ile  
 165 170 175  
 Arg Arg Cys Val Leu Phe Ser Tyr Asn Pro Asp Thr Lys Leu Val Glu  
 180 185 190  
 Met Pro His Tyr Ser Val Gln Val Val Pro Val Gly Leu Lys Arg Ala  
 195 200 205  
 Val Gln Lys Ile Val Lys Gly Thr Val Pro Asn Leu Gly Lys Cys Asn  
 210 215 220  
 Glu Val Val Asp Phe Val Thr Lys Asp Gly Tyr Ala Ser Glu Ser Glu  
 225 230 235 240  
 Ala Glu Asp Asp Glu Gln Ser His Val Val Leu Ala Gln Thr Leu Lys  
 245 250 255  
 Ser Lys Gly Asn Leu Glu Asp Lys Lys Ser Ser Ile Lys Leu His Glu  
 260 265 270

```

Ile Gly Pro Arg Leu Thr Met Gln Leu Ile Lys Ile Glu Glu Gly Leu
      275          Leu      280 Cys      285
Leu Thr Gly Glu Val Ile Tyr His Asp His Val Val Lys Thr Glu Asp
      290          295          300
Glu Lys Glu Thr Leu Arg Lys Leu Val Glu Lys Lys Arg Lys Gln Lys
305          310          315 Phe      320
Glu Gln Arg Lys Lys Glu Gln Ala Glu Asn Arg Ala Arg Asn Leu Lys
      325          330          335
Leu Lys Lys Asp Glu Lys Trp Ala Ala Lys Arg Ala Ala Glu Gly Arg
      340          345          350
Thr Asp Ser Asp Pro Glu Asp Asp Ala Glu Tyr Tyr Lys Glu Glu Val
      355          360          365
Gly Glu Glu Pro Asp Glu Glu Leu Phe Lys Met Glu Ala Lys Ser Ser
      370          375          380
Arg Lys Arg Pro Ser Leu Gly Gly Gly Met Lys Tyr Lys Asn Lys Arg
385          390          395
Ala Lys Leu Asp Thr Lys Asp Lys Asn Asp Lys Ser Glu Arg Thr Asp
Phe          405 Cys          410          415
Lys Tyr Asp Arg Lys Asp Lys Phe Asp Arg Lys Asp Lys Lys Asp Lys
      420          425          430
Phe Asp Pro Lys Asn Gly Arg Ala Lys Phe Asp Pro Lys Asn Lys Arg
      435          440          445
Ala Lys Phe Asp His Arg Lys Ser Arg Lys Ser Lys
      450          455          460

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<210> 18

<211> 15

<212> DNA

<213> homo sapien

<400> 18

agggcgctcgg ggagg

15

<210> 19

<211> 358

<212> PRT

<213> mus musulus

<220>

<221> VARIANT

<222> (1) ... (358)

<223> Xaa = Any Amino Acid

<400> 19

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Phe Gly Gln Gly Gly Lys Gln Ala Ala Trp Gly Ser Pro Gly Gly Pro
  1              5              10              15
Asp Ile Arg Ser Ala Ile Ala Pro Gly Glu Leu Arg Asn Leu Glu Ser
      20              25              30
Tyr Ala Ala Gln Pro His Ser Phe Val Phe Thr Arg Gly Arg Ala Gly
      35              40              45
Arg Asn Val Arg Gln Leu Ser Leu Asp Val Arg Arg Val Met Glu Pro
      50              55              60
Leu Thr Ala Thr Arg Leu Gln Val Arg Lys Lys Asn Ser Leu Lys Asp

```

```

65          70          75          80
Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His Phe Leu Ile Leu
          85          90          95
Thr Lys Thr Asp Asn Ser Val Tyr Leu Lys Leu Met Arg Leu Pro Gly
          100          105          110
Gly Pro Thr Leu Thr Phe Gln Ile Ser Lys Tyr Thr Leu Ile Arg Asp
          115          120          125
Val Val Ser Ser Leu Arg Arg His Arg Met His Glu Gln Gln Phe Asn
          130          135          140
His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro Gln Gly Met Lys
145          150          155          160
Ile Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe Pro Ser Ile Asn
          165          170          175
Val His Thr Val Asn Leu Asn Thr Ile Lys Arg Cys Leu Leu Ile Asn
          180          185          190
Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His Tyr Ser Val Lys
          195          200          205
Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys Leu Leu Gln Glu
          210          215          220
Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser Glu Leu Leu Ala
225          230          235          240
Thr Gly Val Gly Leu Ser Asp Ser Glu Val Glu Pro Asp Gly Glu His
          245          250          255
Asn Thr Thr Glu Leu Pro Gln Ala Val Ala Gly Arg Gly Asn Met Gln
          260          265          270
Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly Pro Arg Met Thr
          275          280          285
Leu Gln Leu Ile Lys Ile Gln Glu Gly Val Gly Asn Gly Asn Val Leu
          290          295          300
Phe His Ser Phe Val His Lys Thr Glu Glu Glu Leu Gln Ala Ile Leu
305          310          315          320
Ala Ala Lys Glu Glu Lys Leu Arg Leu Lys Ala Gln Arg Gln Asn Gln
          325          330          335
Gln Ala Glu Asn Leu Gln Arg Xaa Arg Ser Cys Arg Xaa Pro Thr Arg
          340          345          350
Arg Arg Ala Trp Gln Ala
          355

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<210> 20  
 <211> 137  
 <212> PRT  
 <213> homo sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(137)  
 <223> Xaa = Any Amino Acid

<400> 20

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Leu Gly Pro Arg Val Thr His Phe Leu Ile Leu Ser Lys Thr Glu Thr
1          5          10          15
Asn Val Tyr Phe Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr
          20          25          30

```



4  
Phe Gln Val Lys Lys Tyr Ser Leu Val Arg Asp Val Val Ser Ser Leu  
7 35 40 45  
Arg Arg His Arg Met His Glu Gln Gln Phe Ala His Pro Pro Leu Leu  
50 55 60  
Val Leu Asn Ser Phe Gly Pro His Gly Met His Val Lys Leu Met Ala  
65 70 75 80  
Thr Met Phe Gln Asn Leu Phe Pro Ser Ile Asn Val His Lys Val Asn  
85 90 95  
Leu Asn Thr Ile Lys Arg Cys Ser Ser Xaa Asp Leu Lys Pro Gly Phe  
100 105 110  
Pro Arg Ser Leu Asp Phe Arg Pro Ile Ile Ala Phe Lys Gly Gly Ser  
115 120 125  
Cys Trp Ala Pro Asn Ser Gly Gly Leu  
130 135